

1653  
1600439RECEIVED  
JUN 04 2002  
TECH CENTER 1600/2900

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/000,439

DATE: 02/26/2002

TIME: 13:24:09

Input Set : A:\UC067.004A-SEQ-ID.txt

Output Set: N:\CRF3\02262002\J000439.raw

ENTERED

4 <110> APPLICANT: Saxon, Andrew  
 6 <120> TITLE OF INVENTION: FUSION MOLECULES AND METHODS FOR  
 7 TREATMENT OF IMMUNE DISEASES  
 10 <130> FILE REFERENCE: UC067.004A  
 12 <140> CURRENT APPLICATION NUMBER: US 10/000,439  
 13 <141> CURRENT FILING DATE: 2001-10-24  
 15 <150> PRIOR APPLICATION NUMBER: US 09/847,208  
 16 <151> PRIOR FILING DATE: 2001-05-01  
 18 <160> NUMBER OF SEQ ID NOS: 13  
 20 <170> SOFTWARE: FastSEQ for Windows Version 4.0  
 22 <210> SEQ ID NO: 1  
 23 <211> LENGTH: 696  
 24 <212> TYPE: DNA  
 25 <213> ORGANISM: Homo sapiens  
 27 <400> SEQUENCE: 1  
 28 gagcccaaat cttgtgacaa aactcacaca tgcccaccgt gccagcacc tgaactcctg 60  
 29 gggggaccgt cagtcttctt cttcccccca aaacccaagg acaccctcat gatctcccg 120  
 30 acccctgagg tcacatgcgt ggtggtggac gtgagccacg aagaccctga ggtcaagttc 180  
 31 aactggtacg tggacggcgt ggaggtgcat aatgttaaga caaagccgcg ggaggagcag 240  
 32 tacaacagca cgtaccgtgt ggtcagcgtc ctcaccgtcc tgcaccagaa ctggatgaat 300  
 33 ggaaaggagt acaagtgcaa ggtctccaac aaagccctcc cagcccccat cgagaaaacc 360  
 34 atctccaaag ccaaagtga gccccgagaa ccacaggtgt acaccctgcc cccatcccg 420  
 35 gatgagctga ccaagaacca ggtcagcctg acctgcctgg tcaaaggctt ctatccagc 480  
 36 gacatcgccg tggagtggga gagcaatggg cagccggaga acaactacaa gaccagcct 540  
 37 cccgtgctgg actccgctcg ctccttcttc ctctacagca agctcaccgt ggacaagagc 600  
 38 aggtggcagc aggggaacgt cttctcatgc tccgtgatgc atgaggctct gcacaaccac 660  
 39 taccagcaga ggagcctctc cctgtctccg ggtaaa 696  
 41 <210> SEQ ID NO: 2  
 42 <211> LENGTH: 330  
 43 <212> TYPE: PRT  
 44 <213> ORGANISM: Homo sapiens  
 46 <400> SEQUENCE: 2  
 47 Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys  
 48 1 5 10 15  
 49 Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr  
 50 20 25 30  
 51 Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser  
 52 35 40 45  
 53 Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser  
 54 50 55 60  
 55 Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr  
 56 65 70 75 80  
 57 Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys

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58          85          90          95
59 Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys
60          100          105          110
61 Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro
62          115          120          125
63 Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys
64          130          135          140
65 Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp
66 145          150          155          160
67 Tyr Val Asp Gly Val Glu Val His Asn Val Lys Thr Lys Pro Arg Glu
68          165          170          175
69 Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu
70          180          185          190
71 His Gln Asn Trp Met Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn
72          195          200          205
73 Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Val
74          210          215          220
75 Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu
76 225          230          235          240
77 Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr
78          245          250          255
79 Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn
80          260          265          270
81 Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Val Gly Ser Phe Phe
82          275          280          285
83 Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn
84          290          295          300
85 Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Gln
86 305          310          315          320
87 Gln Arg Ser Leu Ser Leu Ser Pro Gly Lys
88          325          330
91 <210> SEQ ID NO: 3
92 <211> LENGTH: 232
93 <212> TYPE: PRT
94 <213> ORGANISM: Homo sapiens
96 <400> SEQUENCE: 3
97 Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
98 1          5          10          15
99 Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
100          20          25          30
101 Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
102          35          40          45
103 Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
104          50          55          60
105 Asp Gly Val Glu Val His Asn Val Lys Thr Lys Pro Arg Glu Glu Gln
106 65          70          75          80
107 Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
108          85          90          95
109 Asn Trp Met Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala

```

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```

110          100          105          110
111 Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Val Gln Pro
112          115          120          125
113 Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr
114          130          135          140
115 Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser
116 145          150          155          160
117 Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
118          165          170          175
119 Lys Thr Thr Pro Pro Val Leu Asp Ser Val Gly Ser Phe Phe Leu Tyr
120          180          185          190
121 Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe
122          195          200          205
123 Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Gln Gln Arg
124          210          215          220
125 Ser Leu Ser Leu Ser Pro Gly Lys
126 225          230
129 <210> SEQ ID NO: 4
130 <211> LENGTH: 1445
131 <212> TYPE: DNA
132 <213> ORGANISM: Homo sapiens
134 <400> SEQUENCE: 4
135 tccacacaga gccatccgt cttccccttg acccgctgct gcaaaaacat tccctccaat 60
136 gccacctcgg tgactctggg ctgcctggcc acgggctact tcccgaggcc ggtgatggtg 120
137 acctgggaca caggctccct caacgggaca actatgacct taccagccac caccctcacg 180
138 ctctctgggtc actatgccac catcagcttg ctgaccgtct cgggtgcgtg ggccaagcag 240
139 atgttcacct gccgtgtggc acacactcca tcgtccacag actgggtcga caacaaaacc 300
140 ttcagcgtct gctccaggga cttcaccccg ccacccgtga agatcttaca gtctctctgc 360
141 gacggcgggcg ggcacttccc cccgaccatc cagctcctgt gcctcgtctc tgggtacacc 420
142 ccagggaacta tcaacatcac ctggctggag gacgggcagg tcatggacgt ggacttgtcc 480
143 accgcctcta ccacgcagga gggtagctg gcctccacac aaagcgagct caccctcagc 540
144 cagaagcact ggctgtcaga ccgcacctac acctgccagg tcacctatca aggtcacacc 600
145 tttgaggaca gcaccaagaa gtgtgcagat tccaaccoga gaggggtgag cgcctacctc 660
146 agccggccca gcccgttcga cctgttcac cgaagtcgc ccacgatcac ctgtctgggtg 720
147 gtggacctgg caccagcaa ggggaccgtg aacctgacct ggtcccgggc cagtgggaag 780
148 cctgtgaacc actccaccag aaaggaggag aagcagcgca atggcacgtt aaccgtcacg 840
149 tccacctgc cggtgggcac ccgagactgg atcgaggggg agacctacca gtgcagggtg 900
150 acccaccccc acctgccag ggcctcatg cgggccacga ccaagaccag cggcccgcgt 960
151 gctgcccccg aagtctatgc gtttgcgacg ccggagtggc cggggagccg ggacaagcgc 1020
152 accctcgcct gcctgatcca gaacttcatg cctgaggaca tctcggtgca gtggctgcac 1080
153 aacgaggtgc agtcccga cgcgccgcac agcacgacgc agccccgcaa gaccaagggc 1140
154 tccggtctct tcgtcttcag ccgcctggag gtgaccaggg ccgaatggga gcagaaagat 1200
155 gagttcatct gccgtgcagt ccatgaggca gcgagccct cacagaccgt ccagcgagcg 1260
156 gtgtctgtaa atcccggtaa atgacgtact cctgcctccc tccctcccag ggctccatcc 1320
157 agctgtgcag tggggaggac tggccagacc ttctgtccac tgttgcaatg accccaggaa 1380
158 gctaccccca ataaactgtg cctgtcaga gccccagtag acccattctt gggagcgggc 1440
159 aggc
161 <210> SEQ ID NO: 5
162 <211> LENGTH: 427

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163 <212> TYPE: PRT
164 <213> ORGANISM: Homo sapiens
166 <400> SEQUENCE: 5
167 Ser Thr Gln Ser Pro Ser Val Phe Pro Leu Thr Arg Cys Cys Lys Asn
168 1 5 10 15
169 Ile Pro Ser Asn Ala Thr Ser Val Thr Leu Gly Cys Leu Ala Thr Gly
170 20 25 30
171 Tyr Phe Pro Glu Pro Val Met Val Thr Trp Asp Thr Gly Ser Leu Asn
172 35 40 45
173 Gly Thr Thr Met Thr Leu Pro Ala Thr Thr Leu Thr Leu Ser Gly His
174 50 55 60
175 Tyr Ala Thr Ile Ser Leu Leu Thr Val Ser Gly Ala Trp Ala Lys Gln
176 65 70 75 80
177 Met Phe Thr Cys Arg Val Ala His Thr Pro Ser Ser Thr Asp Trp Val
178 85 90 95
179 Asp Asn Lys Thr Phe Ser Val Cys Ser Arg Asp Phe Thr Pro Pro Thr
180 100 105 110
181 Val Lys Ile Leu Gln Ser Ser Cys Asp Gly Gly Gly His Phe Pro Pro
182 115 120 125
183 Thr Ile Gln Leu Leu Cys Leu Val Ser Gly Tyr Thr Pro Gly Thr Ile
184 130 135 140
185 Asn Ile Thr Trp Leu Glu Asp Gly Gln Val Met Asp Val Asp Leu Ser
186 145 150 155 160
187 Thr Ala Ser Thr Thr Gln Glu Gly Glu Leu Ala Ser Thr Gln Ser Glu
188 165 170 175
189 Leu Thr Leu Ser Gln Lys His Trp Leu Ser Asp Arg Thr Tyr Thr Cys
190 180 185 190
191 Gln Val Thr Tyr Gln Gly His Thr Phe Glu Asp Ser Thr Lys Lys Cys
192 195 200 205
193 Ala Asp Ser Asn Pro Arg Gly Val Ser Ala Tyr Leu Ser Arg Pro Ser
194 210 215 220
195 Pro Phe Asp Leu Phe Ile Arg Lys Ser Pro Thr Ile Thr Cys Leu Val
196 225 230 235 240
197 Val Asp Leu Ala Pro Ser Lys Gly Thr Val Asn Leu Thr Trp Ser Arg
198 245 250 255
199 Ala Ser Gly Lys Pro Val Asn His Ser Thr Arg Lys Glu Glu Lys Gln
200 260 265 270
201 Arg Asn Gly Thr Leu Thr Val Thr Ser Thr Leu Pro Val Gly Thr Arg
202 275 280 285
203 Asp Trp Ile Glu Gly Glu Thr Tyr Gln Cys Arg Val Thr His Pro His
204 290 295 300
205 Leu Pro Arg Ala Leu Met Arg Ser Thr Thr Lys Thr Ser Gly Pro Arg
206 305 310 315 320
207 Ala Ala Pro Glu Val Tyr Ala Phe Ala Thr Pro Glu Trp Pro Gly Ser
208 325 330 335
209 Arg Asp Lys Arg Thr Leu Ala Cys Leu Ile Gln Asn Phe Met Pro Glu
210 340 345 350
211 Asp Ile Ser Val Gln Trp Leu His Asn Glu Val Gln Leu Pro Asp Ala
212 355 360 365

```

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```

213 Arg His Ser Thr Thr Gln Pro Arg Lys Thr Lys Gly Ser Gly Phe Phe
214      370      375      380
215 Val Phe Ser Arg Leu Glu Val Thr Arg Ala Glu Trp Glu Gln Lys Asp
216 385      390      395      400
217 Glu Phe Ile Cys Arg Ala Val His Glu Ala Ala Ser Pro Ser Gln Thr
218      405      410      415
219 Val Gln Arg Ala Val Ser Val Asn Pro Gly Lys
220      420      425
223 <210> SEQ ID NO: 6
224 <211> LENGTH: 320
225 <212> TYPE: PRT
226 <213> ORGANISM: Homo sapiens
228 <400> SEQUENCE: 6
229 Phe Thr Pro Pro Thr Val Lys Ile Leu Gln Ser Ser Cys Asp Gly Gly
230 1      5      10      15
231 Gly His Phe Pro Pro Thr Ile Gln Leu Leu Cys Leu Val Ser Gly Tyr
232      20      25      30
233 Thr Pro Gly Thr Ile Asn Ile Thr Trp Leu Glu Asp Gly Gln Val Met
234      35      40      45
235 Asp Val Asp Leu Ser Thr Ala Ser Thr Thr Gln Glu Gly Glu Leu Ala
236      50      55      60
237 Ser Thr Gln Ser Glu Leu Thr Leu Ser Gln Lys His Trp Leu Ser Asp
238 65      70      75      80
239 Arg Thr Tyr Thr Cys Gln Val Thr Tyr Gln Gly His Thr Phe Glu Asp
240      85      90      95
241 Ser Thr Lys Lys Cys Ala Asp Ser Asn Pro Arg Gly Val Ser Ala Tyr
242      100      105      110
243 Leu Ser Arg Pro Ser Pro Phe Asp Leu Phe Ile Arg Lys Ser Pro Thr
244      115      120      125
245 Ile Thr Cys Leu Val Val Asp Leu Ala Pro Ser Lys Gly Thr Val Asn
246      130      135      140
247 Leu Thr Trp Ser Arg Ala Ser Gly Lys Pro Val Asn His Ser Thr Arg
248 145      150      155      160
249 Lys Glu Glu Lys Gln Arg Asn Gly Thr Leu Thr Val Thr Ser Thr Leu
250      165      170      175
251 Pro Val Gly Thr Arg Asp Trp Ile Glu Gly Glu Thr Tyr Gln Cys Arg
252      180      185      190
253 Val Thr His Pro His Leu Pro Arg Ala Leu Met Arg Ser Thr Thr Lys
254      195      200      205
255 Thr Ser Gly Pro Arg Ala Ala Pro Glu Val Tyr Ala Phe Ala Thr Pro
256      210      215      220
257 Glu Trp Pro Gly Ser Arg Asp Lys Arg Thr Leu Ala Cys Leu Ile Gln
258 225      230      235      240
259 Asn Phe Met Pro Glu Asp Ile Ser Val Gln Trp Leu His Asn Glu Val
260      245      250      255
261 Gln Leu Pro Asp Ala Arg His Ser Thr Thr Gln Pro Arg Lys Thr Lys
262      260      265      270
263 Gly Ser Gly Phe Phe Val Phe Ser Arg Leu Glu Val Thr Arg Ala Glu
264      275      280      285

```

Use of n and / or Xaa has been detected in the Sequence Listing. Review the Sequence Listing to ensure a corresponding explanation is present in the <220> to <223> fields of each sequence using n or Xaa.

## VERIFICATION SUMMARY

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L:389 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10  
L:391 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10  
L:406 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11  
L:408 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11